



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 162588

TO: Vanessa L Ford
Location: rem/3B25/3C18
Art Unit: 1645
Tuesday, August 16, 2005

Case Serial Number: 09/884465

From: Mary Jane Ruhl
Location: Biotech-Chem Library
Remsen 1-A-62
Phone: 571-272-2524

maryjane.ruhl@uspto.gov

Search Notes

Examiner Ford,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl
Technical Information Specialist
STIC
Remsen 1-A-62
Ext. 22524



From: Chan, Christina
Sent: Monday, August 15, 2005 6:57 PM
To: Ford, Vanessa; STIC-Biotech/ChemLib
Subject: RE: in re: 09/884465 sequence search

Please rush. Thanks Chris

Chris Chan
SPE, 1644
TC 1600 New Hire Training Coordinator
571-272-0841
Remsen 3E89

-----Original Message-----

From: **Ford, Vanessa**
Sent: Monday, August 15, 2005 6:42 PM
To: Chan, Christina
Subject: in re: 09/884465 sequence search

Please search SEQ ID NO:332. Please include interference searches. Please rush. Please provide at least 60 hits.

Vanessa L. Ford
Biotechnology Patent Examiner
Office: REM 3B25
Mailbox: REM 3C18
Phone: 571.272.0857
art unit:1645

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIS: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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OM protein - protein search, using sw model

Run on: August 16, 2005, 10:23:21 / Search time 26 Seconds
(without alignments)

2601.233 Million cell updates/sec

Title: US-09-884-465A-332
Perfect score: 4728
Sequence: 1 MQITTYDDDEIQVAKAGKYT.....IBRLPGEVYKKNLSPDPIA 906

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 180 summaries

Database:

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2: /cgn2_6/ptodata/1/1aa/5B_COMB.rep: *
3: /cgn2_6/ptodata/1/1aa/6A_COMB.rep: *
4: /cgn2_6/ptodata/1/1aa/6B_COMB.rep: *
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.rep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.rep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3375	71.4	1039	4 US-09-583-110-5226	Sequence 5226, Ap
2	3280	69.4	708	4 US-09-107-433-4231	Sequence 4231, Ap
3	1314.5	27.8	678	4 US-09-107-433-4992	Sequence 4992, Ap
4	1314.5	27.8	838	4 US-09-583-110-5225	Sequence 5225, Ap
5	1302.5	27.5	838	4 US-09-468-656A-4	Sequence 4, Appl1
6	946	20.0	830	4 US-09-107-433-3309	Sequence 4309, Ap
7	946	20.0	851	4 US-09-583-110-3850	Sequence 3850, Ap
8	937.5	19.8	819	4 US-09-468-656A-10	Sequence 10, Appl1
9	818.5	17.3	763	3 US-08-961-083-66	Sequence 66, Appl1
10	818.5	17.3	763	4 US-09-536-784-66	Sequence 66, Appl1
11	637	13.5	819	4 US-09-468-656A-8	Sequence 8, Appl1
12	636	13.5	796	3 US-08-961-083-56	Sequence 56, Appl1
13	636	13.5	796	4 US-09-536-784-56	Sequence 56, Appl1
14	636	13.5	816	4 US-09-645-835A-7	Sequence 7, Appl1
15	635	13.4	321	4 US-09-107-433-3993	Sequence 2893, Ap
16	631	13.3	829	4 US-09-583-110-3851	Sequence 3851, Ap
17	470	9.9	484	4 US-09-468-656A-6	Sequence 6, Appl1
18	431	9.1	447	3 US-08-961-083-182	Sequence 182, App
19	431	9.1	447	4 US-09-536-784-182	Sequence 182, Appl1
20	230	4.9	825	4 US-09-645-835A-2	Sequence 2, Appl1
21	223.5	4.7	822	3 US-09-645-835A-6	Sequence 6, Appl1
22	223.5	4.7	10182	3 US-09-134-001C-3159	Sequence 3159, Ap
23	217.5	4.6	5024	4 US-09-710-279-9964	Sequence 2964, Ap
24	199.5	4.2	1098	3 US-08-923-992A-8	Sequence 8, Appl1
25	195.5	4.1	1128	3 US-08-923-992A-6	Sequence 6, Appl1
26	194.5	4.1	1164	3 US-08-923-992A-2	Sequence 2, Appl1
27	192	4.1	571	3 US-08-961-083-4	Sequence 4, Appl1

28	192	4.1	571	4 US-09-536-784-4	Sequence 4, Appl1
29	192	4.1	1164	3 US-08-923-992A-10	Sequence 10, Appl1
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36	184.5	3.9	1964	2 US-08-790-912-3	Sequence 3, Appl1
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38	184	3.9	8991	4 US-08-714-741-32	Sequence 32, Appl1
39	182	3.8	984	1 US-08-242-932-2	Sequence 2, Appl1
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41	182	3.8	984	5 PCT-US95-06111-2	Sequence 2, Appl1
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44	178	3.8	2753	4 US-09-949-016-7660	Sequence 7660, Ap
45	175.5	3.7	952	4 US-09-107-532A-4706	Sequence 4706, Ap
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49	174	3.7	3924	4 US-09-538-092-1246	Sequence 1246, Ap
50	172.5	3.6	1965	4 US-09-583-110-3829	Sequence 3829, Ap
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52	172	3.6	1279	4 US-09-710-279-3188	Sequence 3188, Ap
53	171	3.6	917	4 US-09-248-796A-18960	Sequence 18960, A
54	171	3.6	1240	4 US-09-538-092-658	Sequence 658, Ap
55	170.5	3.6	1545	3 US-08-296-791-4	Sequence 4, Appl1
56	170.5	3.6	1545	4 US-09-839-996-4	Sequence 4, Appl1
57	170.5	3.6	1545	4 US-10-080-505-4	Sequence 4, Appl1
58	170.5	3.6	1545	4 US-10-080-505-4	Sequence 4, Appl1
59	170.5	3.6	1545	4 US-10-080-505-4	Sequence 4, Appl1
60	170	3.6	1545	5 PCT-US95-10661A-4	Sequence 4, Appl1
61	170	3.6	1848	3 US-08-296-791-6	Sequence 6, Appl1
62	170	3.6	1848	4 US-09-839-996-6	Sequence 6, Appl1
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67	168.5	3.6	171	4 US-09-107-433-3778	Sequence 3778, Ap
68	168.5	3.6	1315	4 US-09-200-650E-5	Sequence 5, Appl1
69	168.5	3.6	3135	1 US-08-323-170B-2	Sequence 2, Appl1
70	168.5	3.6	3135	3 US-08-323-170B-2	Sequence 2, Appl1
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74	166.5	3.5	160	4 US-09-583-110-5230	Sequence 5230, Ap
75	166.5	3.5	905	4 US-09-248-796A-16333	Sequence 16333, A
76	165.5	3.5	1181	3 US-09-206-898-23	Sequence 23, Appl1
77	165	3.5	1437	4 US-09-949-016-10535	Sequence 10535, A
78	164.5	3.5	962	4 US-09-071-035-246	Sequence 246, Ap
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80	164.5	3.5	962	4 US-09-071-035-254	Sequence 254, Ap
81	164.5	3.5	962	4 US-09-071-035-470	Sequence 470, Ap
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88	163.5	3.5	1881	3 US-09-233-086-3	Sequence 3, Appl1
89	163	3.4	880	4 US-09-583-110-5012	Sequence 5012, Ap
90	162.5	3.4	1781	4 US-09-561-403-13	Sequence 13, Appl1
91	162	3.4	2133	3 US-08-968-685A-10	Sequence 10, Appl1
92	161	3.4	676	3 US-09-134-001C-4318	Sequence 4318, Ap
93	161	3.4	825	4 US-09-248-796A-16538	Sequence 16538, A
94	161	3.4	1167	2 US-08-589-756-2	Sequence 2, Appl1
95	161	3.4	1167	3 US-09-206-898-2	Sequence 2, Appl1
96	161	3.4	1167	3 US-09-206-898-2	Sequence 2, Appl1
97	160.5	3.4	1301	4 US-09-071-035-234	Sequence 234, Ap
98	160.5	3.4	1301	4 US-09-071-035-238	Sequence 238, Ap
99	160.5	3.4	1301	4 US-09-071-035-242	Sequence 242, Ap
100	160.5	3.4	1333	4 US-09-248-796A-15543	Sequence 15543, A

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OM protein - protein search, using sw model

Run on: August 16, 2005, 10:23:20 ; Search time 86 Seconds
(without alignment)

4074.476 Million cell updates/sec

Title: US-09-884-465a-332

Sequence: 1 MGIYTDDEIOVALAGKTT.....TELRPSEGVTKKNSDFIA 906

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 2: Geneseq19908:*
- 3: Geneseq20008:*
- 4: Geneseq20018:*
- 5: Geneseq20028:*
- 6: Geneseq20038:*
- 7: Geneseq20048:*
- 8: Geneseq20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4728	100.0	907	5	AAU84065 S. pneumo
2	4723	99.9	907	5	AAU84061 S. pneumo
3	4705	99.5	907	5	AAU84063 S. pneumo
4	4702.5	99.5	908	7	ABM18896 S. pneumo
5	4693.5	99.3	908	7	ABM18897 S. pneumo
6	4675	98.9	901	5	AAU84067 S. pneumo
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8	4672	98.9	906	8	ADP18483 S. pneumo
9	4672	98.8	908	5	AAU84068 S. pneumo
10	4668.5	98.7	908	7	ABM18903 S. pneumo
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12	4663	98.6	901	5	AAU84072 S. pneumo
13	4661	98.6	918	7	ABM18925 S. pneumo
14	4659.5	98.6	902	7	ABM18879 S. pneumo
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17	4656.5	98.5	902	5	AAU84076 S. pneumo
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21	4653.5	98.4	929	7	ABM18921 S. pneumo
22	4653.5	98.4	931	7	ABM18924 S. pneumo
23	4652.5	98.4	902	5	AAU84078 S. pneumo
24	4650.5	98.4	901	7	ABM18892 S. pneumo
25	4649.5	98.3	925	7	ABM18922 S. pneumo

26	4649.5	98.3	929	7	ABM18920 S. pneumo
27	4634	98.0	938	7	ABM18927 S. pneumo
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62	3359	71.0	1039	8	ADK48711 S. pneumo
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66	3357	71.0	1039	3	AAU84021 S. pneumo
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69	3300.5	69.8	807	5	AAU83997 S. pneumo
70	3300.5	69.8	807	5	ABM18833 S. pneumo
71	3298	69.8	632	5	AAU84009 S. pneumo
72	3298	69.8	633	7	ABM18800 S. pneumo
73	3298	69.8	633	7	ABM18854 S. pneumo
74	3298	69.8	901	5	AAU84066 S. pneumo
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76	3298	69.8	907	5	AAU84064 S. pneumo
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78	3293	69.6	632	5	AAU84013 S. pneumo
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87	3293	69.6	908	7	ABM18898 S. pneumo
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89	3288	69.5	644	5	AAU83998 S. pneumo
90	3288	69.5	644	5	ABM18829 S. pneumo
91	3284	69.5	632	5	AAU84004 S. pneumo
92	3284	69.5	632	5	AAU84004 S. pneumo
93	3284	69.5	632	5	AAU84004 S. pneumo
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96	3284	69.5	633	7	ABM18849 S. pneumo
97	3283	69.4	632	5	AAU84015 S. pneumo
98	3283	69.4	633	7	ABM18852 S. pneumo

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OM protein - protein search, using sw model

Run on: August 16, 2005, 10:23:20 ; Search time 180 Seconds
(without alignments)
2577.465 Million cell updates/sec

Title: US-09-884-465A-332
Perfect score: 4728
Sequence: 1 MGYTDDDEIQVAKLAGXT.....IHLRLPSGVYIKNLSDFIA 906

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 180 summaries

Database : uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
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4	3356	71.0	1039	2	08DQ07 streptococc
5	1307.5	27.7	839	2	06WNP9 streptococc
6	1307.5	27.7	839	2	09ANY2 streptococc
7	1300.5	27.5	816	2	06WNP6 streptococc
8	1300.5	27.5	830	2	06WNP5 streptococc
9	1273.5	26.9	811	2	06WNO0 streptococc
10	1273.5	26.9	825	2	06WNO1 streptococc
11	1249	26.4	834	2	06WNP8 streptococc
12	1245	26.3	853	2	08D008 streptococc
13	946.5	20.0	819	2	097Q09 streptococc
14	946	20.0	807	2	06T304 streptococc
15	946	20.0	811	2	06WNO3 streptococc
16	946	20.0	844	2	09AG74 streptococc
17	946	20.0	855	2	08CWR4 streptococc
18	935.5	19.8	819	2	09ANY3 streptococc
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20	636	13.5	816	2	09AHT9 streptococc
21	636	13.5	817	2	06T8D7 streptococc
22	636	13.5	828	2	08DPO2 streptococc
23	233	4.9	825	2	093G75 streptococc
24	230	4.9	825	2	093XV4 streptococc
25	227	4.8	794	2	0877Y2 streptococc
26	227	4.8	823	2	08K5Q1 streptococc
27	226.5	4.8	822	2	08K4U1 streptococc
28	223.5	4.7	823	2	08N282 streptococc
29	223.5	4.7	822	2	09ZHG7 streptococc
30	223.5	4.7	9439	2	08CFP6 streptococc
31	222.5	4.7	822	2	08D281 streptococc

32	222.5	4.7	9196	2	081Q87 drosophila
33	220.5	4.7	861	2	06VY65 drosophila
34	220	4.7	2762	2	09YGM4 drosophila
35	217.5	4.6	1800	2	081E19 plasmodium
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37	217	4.6	3452	2	081EA3 plasmodium
38	215.5	4.6	1524	2	08ARN2 plasmodium
39	213.5	4.5	5458	2	09U459 plasmodium
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41	212.5	4.5	3507	2	081HN3 plasmodium
42	212	4.5	3471	2	06HMX5 bacillus th
43	211.5	4.5	3455	2	06RS49 tenebrio mo
44	211	4.5	2042	2	06BU09 debaryomyce
45	210.5	4.5	1785	2	06RS79 candida gla
46	208.5	4.4	1206	2	0895S7 clostridium
47	208	4.4	2647	2	09U4X0 plasmodium
48	207.5	4.4	1409	2	07RK24 plasmodium
49	207	4.4	1417	2	0871Y7 neurospora
50	206.5	4.4	3472	2	0632D5 bacillus ce
51	205.5	4.3	3392	2	07EAD9 ashbya gos
52	205.5	4.3	3392	2	07ZK38 ashbya gos
53	204.5	4.3	1083	2	075WB4 saccharomyc
54	204	4.3	1790	1	US01 YEAST
55	204	4.3	3404	2	07RUB3 plasmodium
56	203.5	4.3	1675	2	07RHM8 plasmodium
57	203	4.3	3504	2	081I45 plasmodium
58	202.5	4.3	2261	2	07RUS3 plasmodium
59	202.5	4.3	2269	2	026223 plasmodium
60	201.5	4.3	1078	2	0963T1 plasmodium
61	201.5	4.3	1873	2	09ZAN7 enterococcu
62	201.5	4.3	3373	2	0816D8 bacillus ce
63	201	4.3	1268	2	07IGT1 saccharomyc
64	201	4.3	1790	2	007380 saccharomyc
65	201	4.3	2004	2	097Q7P streptococc
66	200.5	4.2	2582	2	07RK50 plasmodium
67	199.5	4.2	1254	2	07RGT9 plasmodium
68	199.5	4.2	2738	2	081HU4 plasmodium
69	198	4.2	1123	2	06S255 streptococc
70	198	4.2	1420	2	09Y0Y8 drosophila
71	197.5	4.2	3692	2	08CNU9 staphylococc
72	197	4.2	1361	2	07REY0 plasmodium
73	197	4.2	1478	1	BCK1 YEAST
74	197	4.2	2689	2	07RE57 plasmodium
75	197	4.2	2720	2	061WC6 plasmodium
76	197	4.2	18519	2	081SP6 caenorhabdi
77	197	4.2	18534	2	081SP7 caenorhabdi
78	196	4.1	1780	2	06TV07 homo sapien
79	196	4.1	1811	2	07REH9 plasmodium
80	195.5	4.1	1139	2	097237 plasmodium
81	195.5	4.1	1900	2	06VXQ3 enterococcu
82	195.5	4.1	1954	2	07MIT8 vibrio vuln
83	195	4.1	1698	2	091C00 staphylococc
84	195	4.1	2209	2	07AH47 streptococc
85	195	4.1	2910	2	09RND5 arabidopsis
86	194.5	4.1	1134	2	099051 streptococc
87	194.5	4.1	1164	1	BAG STRAG
88	194	4.1	1126	2	08B6U1 streptococc
89	193.5	4.1	1125	2	098PM9 mycoplasma
90	193.5	4.1	1524	2	07RCM2 plasmodium
91	193.5	4.1	3869	2	07RNB4 plasmodium
92	193	4.1	1245	2	09I470 staphylococc
93	192	4.1	839	2	06G315 bartonella
94	192	4.1	1871	2	09SRD5 arabidopsis
95	192	4.1	3009	2	07RG00 plasmodium
96	191.5	4.1	1906	2	0813H0 plasmodium
97	191	4.0	1534	2	09VEH3 drosophila
98	191	4.0	3111	2	09VH10 drosophila
99	191	4.0	5251	2	081ID4 plasmodium
100	190.5	4.0	1158	2	06J5M4 streptococc
101	190.5	4.0	2095	2	07RN75 plasmodium
102	190.5	4.0	2276	2	0791N3 staphylococc
103	190.5	4.0	2747	2	09BUX9 plasmodium
104	190	4.0	1596	2	062766 rattus norv

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OM protein - protein search, using sw model

Run on: August 16, 2005, 10:23:21 ; Search time 24 Seconds
(without alignments)
3632.183 Million cell updates/sec

Title: US-09-884-465a-332
Perfect score: 4728

Sequence: 1 MGIITDDEIQVAKLAGKYT.....IELRLPSGEVKKNSDFIA 906

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 180 summaries

Database : PIR 79:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3357	71.0	1039	2 H95115	conserved hypotet
2	3356	71.0	1039	2 D97985	hypothetical prote
3	1307.5	27.7	839	2 G95115	conserved hypotet
4	1245	26.3	853	2 C97985	hypothetical prote
5	946.5	20.0	819	2 B95136	conserved domain p
6	946	20.0	855	2 D98004	histidine Motif-Co
7	636	13.5	802	2 C95136	conserved domain p
8	636	13.5	828	2 B98004	hypothetical prote
9	223.5	4.7	822	2 T67578	hypothetical 92.4K
10	202.5	4.3	822	2 T67578	hypothetical 92.4K
11	201.5	4.3	1873	2 T30944	surface protein pr
12	201	4.3	1790	2 P67593	transport protein
13	201	4.3	2004	2 P95133	immunoglobulin A1
14	197	4.2	1478	2 T20117	protein kinase BCK
15	197	4.2	3488	2 T34418	hypothetical prote
16	194.5	4.1	1134	2 A60234	hypothetical prote
17	194.5	4.1	1164	2 FCS0AG	IgA Fc receptor pr
18	193.5	4.1	1125	2 B90598	membrane nucleas
19	192	4.1	1871	2 F82885	probable heat shoc
20	190	4.0	4688	2 S57976	hypothetical prote
21	189.5	4.0	2748	2 P82884	nuclear migration
22	189.5	4.0	5005	2 P82884	hypothetical prote
23	189.5	4.0	5327	2 T13564	microtubule-associ
24	186	3.9	1640	2 A24594	probable major sur
25	186	3.9	1658	2 S55101	hypothetical prote
26	185.5	3.9	1983	2 G86643	hypothetical prote
27	185.5	3.9	2109	2 B89066	protein H05009.1 (
28	185.5	3.9	2109	2 T33247	hypothetical prote
29	185	3.9	2485	1 H71621	serine/threonine-B

30	184.5	3.9	1963	2 B98002	IgA-specific metal
31	183	3.9	2218	2 B84683	hypothetical prote
32	182	3.8	2450	2 S71625	protein-tyrosine-p
33	181.5	3.8	1139	1 B64234	cytochrome-c-acc
34	181	3.8	1939	2 T18372	repet organellar
35	181	3.8	1979	2 W06059	repeat protein - mo
36	181	3.8	2481	2 D90011	fibin protein (limp
37	180.5	3.8	1185	2 A42404	collagen adhesin -
38	180	3.8	1271	2 A45555	glutamate rich pro
39	180	3.8	1639	2 S05603	major merizote su
40	179.5	3.8	2447	2 T16870	hypothetical prote
41	179	3.8	1969	2 T38495	hypothetical prote
42	178.5	3.8	763	2 T08929	hypothetical prote
43	177.5	3.8	1881	2 H45076	zinc metalloprotei
44	177	3.7	1305	2 H41662	150K mating aggreg
45	176.5	3.7	2195	2 S61103	SEC16 protein - ye
46	176.5	3.7	2484	2 T26216	hypothetical prote
47	176.5	3.7	2607	2 T26215	hypothetical prote
48	175.5	3.7	1036	2 T30311	S-layer protein -
49	175.5	3.7	1086	2 S16752	major merizote su
50	175.5	3.7	1231	2 T28681	rib protein - Stre
51	174.5	3.7	1230	2 T2458	hypothetical prote
52	174	3.7	639	2 S20887	acta protein precu
53	174	3.7	1180	2 T20773	hypothetical prote
54	174	3.7	1526	2 A45605	mature-parasite-in
55	174	3.7	3924	2 S37431	ankyrin 2, neuroma
56	174	3.7	4459	2 T20771	hypothetical prote
57	173.5	3.7	710	2 S30154	low-temperature-in
58	173.5	3.7	1071	2 B85343	hypothetical prote
59	173	3.7	3147	2 T18674	hypothetical prote
60	172.5	3.6	1032	2 T30270	major tegumental a
61	172	3.6	1631	1 S420K1	major merizote su
62	171.5	3.6	825	2 S25706	transcription fact
63	171	3.6	1240	2 S52734	hypothetical prote
64	171	3.6	2401	2 T28676	thoptry protein -
65	171	3.6	5170	2 T15348	hypothetical prote
66	170.5	3.6	1545	2 B41859	IgA-specific metal
67	170.5	3.6	1701	2 A54498	major merizote su
68	170	3.6	1127	2 T25804	hypothetical prote
69	169.5	3.6	857	2 B95009	cell wall surface
70	169	3.6	639	2 A81100	actin-assembly ind
71	168.5	3.6	1020	2 T29108	hypothetical prote
72	168.5	3.6	1315	2 T28679	fibrogen-binding
73	168.5	3.6	3135	2 A48584	transmission block
74	168	3.6	1138	2 H86201	hypothetical prote
75	167.5	3.5	1726	1 S420K1	major merizote su
76	166.5	3.5	1233	2 S59621	hypothetical prote
77	166.5	3.5	1612	2 S59669	DNA topoisomerase
78	166.5	3.5	1701	2 A26868	major merizote su
79	166	3.5	182	2 P97985	hypothetical prote
80	166	3.5	1516	2 G64242	cytochrome-acc
81	165.5	3.5	725	2 T21363	hypothetical prote
82	165	3.5	1650	2 T18444	hypothetical prote
83	165	3.5	1849	2 A41859	IgA-specific metal
84	164.5	3.5	1726	2 C90593	hypothetical prote
85	164.5	3.5	1272	2 A59498	major merizote su
86	164.5	3.5	1952	2 T48814	hypothetical prote
87	164.5	3.5	3381	2 T42389	hypothetical prote
88	164	3.5	1948	2 S00485	hypothetical prote
89	163.5	3.5	2829	2 A42771	reticulocyte-bind
90	163	3.4	1385	2 D89824	hypothetical prote
91	163	3.4	1466	2 A36426	SP2 protein - yea
92	163	3.4	1816	2 F83901	hypothetical prote
93	163	3.4	1837	2 T41023	probable nuclear p
94	163	3.4	2774	2 A43359	microtubule-associ
95	162.5	3.4	766	1 S61694	floculation suppr
96	162.5	3.4	1368	2 T18371	probable glutamate
97	162.5	3.4	1876	2 B97944	zinc metalloprotei
98	162.5	3.4	2144	2 A97942	metalloprotease
99	162.5	3.4	26926	1 I38344	titin, cardiac mus
100	162	3.4	1161	2 C97881	conserved hypotet
101	161.5	3.4	1080	2 T43164	IACa protein - I4
102	161.5	3.4	1252	2 B42771	reticulocyte-bind